Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application.

Listing of Claims:

Claims 1-40 (Cancelled)

41. (New) An isolated nucleic acid molecule comprising a sequence of about the maximum number of nucleotides of a spacer region between:

the large sub-unit and the small sub-unit of rRNA genes of a non-viral organism;

the large sub-unit and the 5S sub-unit of the rRNA genes of a non-viral organism; or

the RNA form thereof.

42. (New) The isolated nucleic acid molecule according to claim 41, wherein the isolated nucleic acid molecule does not include tRNA genes.

43. (New) An isolated nucleic acid molecule comprising an oligonucleotide of about 15 to about 100 contiguous nucleotides from a spacer region between:

the large sub-unit and the small sub-unit of rRNA genes of a non-viral organism;

the large sub-unit and the 5S sub-unit of the rRNA genes of a non-viral organism; or

the RNA form thereof;

said oligonucleotide being able to hybridize specifically to a target, wherein said target does not include tRNA genes.

44. (New) An isolated nucleic acid molecule according to claim 41, wherein the non-viral organism is an eukaryote.

45. (New) An isolated nucleic acid molecule according to claim 43, wherein the non-viral organism is an eukaryote.

46. (New) An isolated nucleic acid molecule according to claim 41, wherein the non-viral organism is a microorganism.

47. (New) An isolated nucleic acid molecule according to claim 43, wherein the non-viral organism is a microorganism.

48. (New) An isolated nucleic acid molecule according to claim 43, wherein the molecule is a probe.

49. (New) An isolated nucleic acid molecule according to claim 43, wherein the molecule is a primer.

50. (New) A method for the detection of a non-viral organisms in a biological sample comprising:

contacting the nucleic acid sequences with at least one probe comprising an oligonucleotide of about 15 to about 100 contiguous nucleotides from a spacer region between:

the large sub-unit and the small sub-unit of rRNA genes of a non-viral organism; or

the RNA form thereof;

at a sufficient temperature and hybridization solution concentration to provide formation of hybrids between a probe and a complementary nucleic acid sequences; and

inferring the presence of said non-viral organism by detecting formation of the hybrids.

51. (New) The method of claim 50, further comprising amplifying the nucleic acid sequences of the biological sample using at least one set of primers derived from a large sub-unit and a small sub-unit.

52. (New) The method according to claim 50, wherein the non-viral organism is an eukaryote.

53. (New) The method according to claim 50, wherein the non-viral organism is microorganism.

54. (New) The method according to claim 51, wherein the amplified product is labeled.

55. (New) The method according to claim 51 wherein the primer is 5' biotinylated.

56. (New) The method according to claim 50, wherein the probe is immobilized on a solid support.

57. (New) The method according to claim 51, further comprising amplifying the nucleic acid sequence of a biological sample using a primer that does not include tRNA genes.

58. (New) The method according to claim 57, wherein the non-viral organism is an eukaryote.

59. (New) The method according to claim 57, wherein the non-viral organism is microorganism.

60. (New) The method according to claim 57, further comprising labeling amplified products obtained from contacting the nucleic acid sequences.

61. (New) The method according to claim 57, wherein the primer is 5' biotinylated.

62. (New) The method according to claim 57, further comprising immobilizing the probe on a solid support.

63. (New) A method for the detection of at least one non-viral organism or for the simultaneous detection of several non-viral organisms comprising:

using a target of an isolated nucleic acid of a sequence of about the maximum number of nucleotides of a spacer region between:

the large sub-unit and the small sub-unit of the rRNA genes of a non-viral organism;

the large sub-unit and the 5S sub-unit of the rRNA genes of a non-viral organism; or

the RNA form thereof;

wherein said target does not include tRNA genes.

64. (New) The method according to claim 63, wherein the non-viral organism is a eukaryote.

65. (New) The method according to claim 63, wherein the non-viral organism is a microorganism.

66. (New) Method according to claim 63, wherein said oligonucleotide is immobilized on a solid support.

67. The method for the detection of at a non-viral organism comprising:

amplifying the nucleic acid sequences of a biological sample using at least one set of primers, wherein the primer comprises an oligonucleotide of about 15 to about 100 contiguous nucleotides from a spacer region between:

the large sub-unit and the small sub-unit of the rRNA genes of a non-viral organism;

the large sub-unit and the 5S sub-unit of the rRNA genes of a non-viral organism; or

the RNA form thereof;

said oligonucleotide being able to hybridize specifically to a target, wherein the target does not include tRNA genes;

sequencing the amplified nucleic acid sequences;

comparing the sequence(s) of the amplified nucleic acids with other nucleic acid sequences; and

inferring the presence of said non-viral organism(s).

68. (New) The method according to claim 67, wherein the non-viral organism is a eukaryote.

69. (New) The method according to claim 67, wherein the non-viral organism is a microorganism.

70. (New) A method for detecting a non-viral organism comprising:

amplifying the nucleic acid sequences of a biological sample using at least one set of primers derived from:

the large sub-unit and the small sub-unit respectively;

or from the large sub-unit and the 5S sub-unit respectively of the rRNA genes of said non-viral organism(s);

sequencing the amplified nucleic acid sequence,

comparing the sequence(s) of the amplified nucleic acids with other nucleic acid sequences, and

inferring the presence of said non-viral organism.

71. (New) The method according to claim 70, wherein said non-viral organism is a eukaryote.

72. (New) The method according to claim 70, wherein said non-viral organism is a microorganism.

73. (New) A method for obtaining a nucleic acid probe, wherein said nucleic acid probe comprises an oligonucleotide of about 15 to about 100 contiguous nucleotides from a spacer region between:

the large sub-unit and the small sub-unit of the rRNA genes of a non-viral organism;

the large sub-unit and the 5S sub-unit of the rRNA genes of a non-viral organism; or

the RNA form thereof;

said oligonucleotide being able to hybridize specifically to a target, said target does not include tRNA genes, the method comprising:

comparing the nucleic acid sequence of the spacer region between the large sub-unit and the small sub-unit, or between the large sub-unit and the 5S sub-unit of the rRNA genes of the sought organism with the nucleic acid sequence of the spacer region between the large sub-unit and the small sub-unit, or between the large sub-unit and the 5S sub-unit of the rRNA genes of the closest neighbors; and

selecting a sequence of about 15 to about 100 nucleotides of the spacer region between the large sub-unit and the small sub-unit, or between the large sub-unit and the 5S sub-unit of the rRNA genes of the sought organism which presents at least one mismatch with the spacer region between the large sub-unit and the small sub-unit, or between the large sub-unit and the 5S sub-unit of the rRNA genes of at least one of the closest neighbors.

74. (New) The method for obtaining a nucleic acid probe, wherein the nucleic acid probe comprises an oligonucleotide of about 15 to about 100 contiguous nucleotides from a spacer region between:

the large sub-unit and the small sub-unit of the rRNA genes of a non-viral organism;

the large sub-unit and the 5S sub-unit of the rRNA genes of a non-viral organism; or

the RNA form thereof;

said oligonucleotide being able to hybridize specifically to a target, said target does not include tRNA genes; the method comprising

deleting, in the spacer region between the large sub-unit and the small sub-unit, or between the large sub-unit and the 5S sub-unit of the rRNA genes of the organism to be sought, the tRNA genes and possibly the signal sequences, to obtain a shortened spacer region, and

determining a specific nucleic acid sequence of about 15 to about 100 nucleotides, from the shortened spacer region, said sequence being able to hybridize specifically with the nucleic acids of the sought organism.

75. (New) A kit for in vitro detection of a non-viral organism comprising:

at least one set of primers, wherein said primer comprises an oligonucleotide of about 15 to about 100 contiguous nucleotides from a spacer region between:

the large sub-unit and the small sub-unit of the rRNA genes of a non-viral organism;

the large sub-unit and the 5S sub-unit of the rRNA genes of a non-viral organism; or

the RNA form thereof;

said oligonucleotide being able to hybridize specifically to a target, wherein the target does not

include tRNA genes;

at least one nucleic acid probe, wherein the probe comprises an oligonucleotide of about

15 to about 100 contiguous nucleotides from a spacer region between:

the large sub-unit and the small sub-unit of the rRNA genes of a non-viral

organism;

the large sub-unit and the 5S sub-unit of the rRNA genes of a non-viral organism; or

or the RNA form thereof;

said oligonucleotide being able to hybridize specifically to a target, said target does not include tRNA genes;

a hybridization buffer, or components for producing the hybridization buffer, the hybridization buffer being effective for forming solution in which said nucleic acid probe(s) can hybridize with said nucleic acid sequences from said non-viral organism(s); and

reagents for detecting the hybrids formed between said nucleic acid probe(s) and said nucleic acid sequences from said non-viral organism(s).

76. (New) A kit for in vitro detection of a non-viral organism comprising:

at least one nucleic acid probe, wherein said probe comprises an oligonucleotide of about 15 to about 100 contiguous nucleotides from a spacer region between:

the large sub-unit and the small sub-unit of rRNA genes of a non-viral organism;

the large sub-unit and the 5S sub-unit of the rRNA genes of a non-viral organism; or

or the RNA form thereof;

said oligonucleotide being able to hybridize specifically to a target, said target does not include tRNA genes;

a hybridization buffer, or components for producing the hybridization buffer, the hybridization buffer being effective for forming solution in which said nucleic acid probe(s) can hybridize with said nucleic acid sequences from said non-viral organism(s); and

reagents for detecting the hybrids formed between said nucleic acid probe(s) and said nucleic acid sequences from said non-viral organism(s).

77. (New) A kit according to claim 75, wherein the non-viral organism is an eukaryote.

78. (New) A kit according to claim 75, wherein the non-viral organism is a microorganism.

79. (New) A kit according to claim 75, further comprising labeling the amplified products.

80. (New) A kit according to claim 75, wherein the primer is 5' biotinylated.

81. (New) A kit according to claim 75, further comprising immobilizing the primer on a solid support.

82. (New) A kit according to claim 76, wherein the non-viral organism is an eukaryote.

83. (New) A kit according to claim 76, wherein the non-viral organism is a microoganism.

84. (New) A kit according to claim 76, further comprising labeling the amplified products.

85. (New) A kit according to claim 76, wherein the primer is 5' biotinylated.

86. (New) A kit according to claim 76, further comprising immobilizing the probe on a solid support.